Figure 1
Sequence of human APRIL (SEQ ID NOS: 1 and 2)

Human G70 cDNA (SEQ ID NO 1)

```
Length: 1465 bp
   1  GCCAACCTTC CCTCCCCCAA CCCTGGGGCC GCCCCAGGGT TCCTGCGCAC
  51  TGCCTGTTCC TCCTGGGTGT CACTGGCAGC CCTGTCCTTC CTAGAGGGAC
 101  TGGAACCTAA TTCTCCTGAG GCTGAGGGAG GGTGGAGGGT CTCAAGGCAA
 151  CGCTGGCCCC ACGACGGAGT GCCAGGAGCA CTAACAGTAC CCTTAGCTTG
 201  CTTTCCTCCT CCCTCCTTTT TATTTTCAAG TTCCTTTTTA TTTCTCCTTG
 251  CGTAACAACC TTCTTCCCTT CTGCACCACT GCCCGTACCC TTACCCGCCC
 301  CGCCACCTCC TTGCTACCCC ACTCTTGAAA CCACAGCTGT TGGCAGGGTC
 351  CCCAGCTCAT GCCAGCCTCA TCTCCTTTCT TGCTAGCCCC CAAAGGGCCT
 401  CCAGGCAACA TGGGGGGCCC AGTCAGAGAG CCGGCACTCT CAGTTGCCCT
 451  CTGGTTGAGT TGGGGGGCAG CTCTGGGGGC CGTGGCTTGT GCCATGGCTC
 501  TGCTGACCCA ACAAACAGAG CTGCAGAGCC TCAGGAGAGA GGTGAGCCGG
 551  CTGCAGGGGA CAGGAGGCCC CTCCCAGAAT GGGGAAGGGT ATCCCTGGCA
 601  GAGTCTCCCG GAGCAGAGTT CCGATGCCCT GGAAGCCTGG GAGAGTGGGG
 651  AGAGATCCCG GAAAAGGAGA GCAGTGCTCA CCCAAAAACA GAAGAAGCAG
 701  CACTCTGTCC TGCACCTGGT TCCCATTAAC GCCACCTCCA AGGATGACTC
 751  CGATGTGACA GAGGTGATGT GGCAACCAGC TCTTAGGCGT GGGAGAGGCC
 801  TACAGGCCCA AGGATATGGT GTCCGAATCC AGGATGCTGG AGTTTATCTG
 851  CTGTATAGCC AGGTCCTGTT TCAAGACGTG ACTTTCACCA TGGGTCAGGT
 901  GGTGTCTCGA GAAGGCCAAG GAAGGCAGGA GACTCTATTC CGATGTATAA
 951  GAAGTATGCC CTCCCACCCG GACCGGGCCT ACAACAGCTG CTATAGCGCA
1001  GGTGTCTTCC ATTTACACCA AGGGGATATT CTGAGTGTCA TAATTCCCCG
1051  GGCAAGGGCG AAACTTAACC TCTCTCCACA TGGAACCTTC CTGGGGTTTG
1101  TGAAACTGTG ATTGTGTTAT AAAAAGTGGC TCCCAGCTTG GAAGACCAGG
1151  GTGGGTACAT ACTGGAGACA GCCAAGAGCT GAGTATATAA AGGAGAGGGA
1201  ATGTGCAGGA ACAGAGGCGT CTTCCTGGGT TTGGCTCCCC GTTCCTCACT
1251  TTTCCCTTTT CATTCCCACC CCCTAGACTT TGATTTTACG GATATCTTGC
1301  TTCTGTTCCC CATGGAGCTC CGAATTCTTG CGTGTGTGTA GATGAGGGGC
1351  GGGGGACGGG CGCCAGGCAT TGTTCAGACC TGGTCGGGGC CCACTGGAAG
1401  CATCCAGAAC AGCACCACCA TCTAACGGCC GCTCGAGGGA AGCACCCGGC
1451  GGTTTGGGCG AAGTC
```

The proposed transmembrane domains are boxed

human G70 protein sequence (SEQ ID NO 2)

```
  1  MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT
 51  QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS
101  RKRRAVLTQK QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA
151  QGYGVRIQDA GVYLLYSQVL FQDVTFTMGQ VVSREGQGRQ ETLFRCIRSM
201  PSHPDRAYNS CYSAGVFHLH QGDILSVIIP RARAKLNLSP HGTFLGFVKL
```

Figure 2A
Sequence of mouse G70 (SEQ ID NOS: 3 and 4)

Mouse G70 (SEQ ID NO 3)

```
1     CATGCCGAGT GCTTTGTGTG TGTTACCTGC TCTAAGAAGC TGGCTGGGCA
51    GCGTTTCACC GCTGTGGAGG ACCAGTATTA CTGCGTGGAT TGCTACAAGA
101   ACTTTGTGGC CAAGAAGTGT GCTGGATGCA AGAACCCCAT CACTGGGTTT
151   GGTAAAGGCT CCAGTGTGGT GGCCTATGAA GGACAATCCT GGCACGACTA
201   CTGCTTCCAC TGCAAAAAAT GCTCCGTGAA TCTGGCCAAC AAGCGCTTTG
251   TATTTCATAA TGAGCAGGTG TATTGCCCTG ACTGTGCCAA AAAGCTGTAA
301   CTTGACGGCT GCCCTGTCCT TCCTAGATAA TGGCACCAAA TTCTCCTGAG
351   GCTAGGGGGG AAGGAGTGTC AGAGTGTCAC TAGCTCGACC CTGGGGACAA
401   GGGGGACTAA TAGTACCCTA GCTTGATTTC TTCCTATTCT CAAGTTCCTT
451   TTTATTTCTC CCTTGCGTAA CCCGCTCTTC CCTTCTGTGC CTTTGCCTGT
501   ATTCCCACCC TCCCTGCTAC CTCTTGGCCA CCTCACTTCT GAGACCACAG
551   CTGTTGGCAG GGTCCCTAGC TCATGCCAGC CTCATCTCCA GGCCACATGG
601   GGGGCTCAGT CAGAGAGCCA GCCCTTTCGG TTGCTCTTTG GTTGAGTTGG
651   GGGGCAGTTC TGGGGGCTGT GACTTGTGCT GTCGCACTAC TGATCCAACA
701   GACAGAGCTG CAAAGCCTAA GGCGGGAGGT GAGCCGGCTG CAGCGGAGTG
751   GAGGGCCTTC CCAGAAGCAG GGAGAGCGCC CATGGCAGAG CCTCTGGGAG
801   CAGAGTCCTG ATGTCCTGGA AGCCTGGAAG GATGGGGCGA AATCTCGGAG
851   AAGGAGAGCA GTACTCACCC AGAAGCACAA GAAGAAGCAC TCAGTCCTGC
901   ATCTTGTTCC AGTTAACATT ACCTCCAAGG ACTCTGACGT GACAGAGGTG
951   ATGTGGCAAC CAGTACTTAG GCGTGGGAGA GGCCTGGAGG CCCAGGGAGA
1001  CATTGTACGA GTCTGGGACA CTGGAATTTA TCTGCTCTAT AGTCAGGTCC
1051  TGTTTCATGA TGTGACTTTC ACAATGGGTC AGGTGGTATC TCGGGAAGGA
1101  CAAGGGAGAA GAGAAACTCT ATTCCGATGT ATCAGAAGTA TGCCTTCTGA
1151  TCCTGACCGT GCCTACAATA GCTGCTACAG TGCAGGTGTC TTTCATTTAC
1201  ATCAAGGGGA TATTATCACT GTCAAAATTC CACGGGCAAA CGCAAAACTT
1251  AGCCTTTCTC CGCATGGAAC ATTCCTGGGG TTTGTGAAAC TATGATTGTT
1301  ATAAAGGGGG TGGGGATTTC CCATTCCAAA AACTGGCTAG ACAAAGGACA
1351  AGGAACGGTC AAGAACAGCT CTCCATGGCT TTGCCTTGAC TGTTGTTCCT
1401  CCCTTTGCCT TTCCCGCTCC CACTATCTGG GCTTTGACTC CATGGATATT
1451  AAAAAAGTAG AATATTTTGT GTTTATCTCC CAAAAA
```

Figure 2B

Mouse G70 Length: 241 (SEQ ID NO 4)

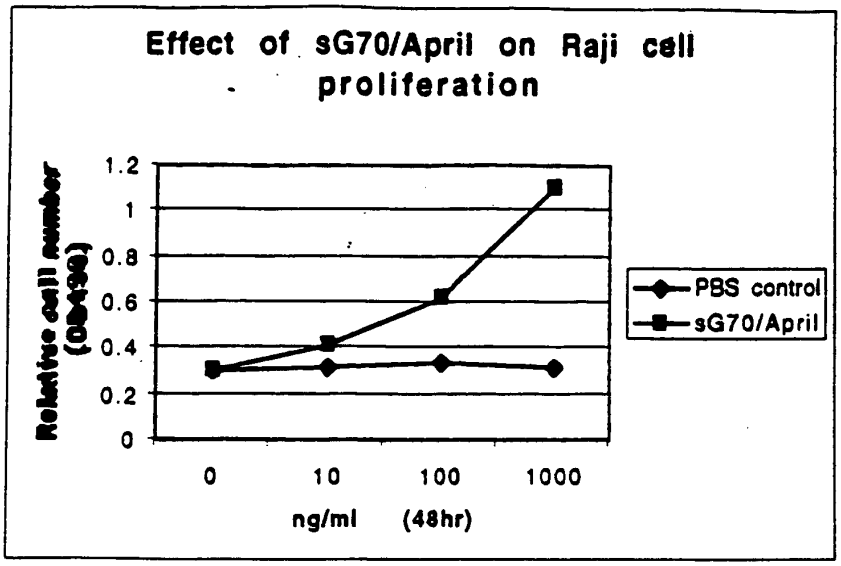
```
  1  MPASSPGHMG GSVREPALSV ALWLSWGAVL GAVTCAVALL IQQTELQSLR
 51  REVSRLQRSG GPSQKQGERP WQSLWEQSPD VLEAWKDGAK SRRRRAVLTQ
101  KHKKKHSVLH EVPVNITSKD SDVTEVMWQP VLRRGRGLEA QGDIVRVWDT
151  GIYLLYSQVL FHDVTFTMGQ VVSREGQGRR ETLFRCIRSM PSDPDRAYNS
201  CYSAGVFHLH QGDIITVKIP RANAKLSLSP HGTFLGFVKL *
```

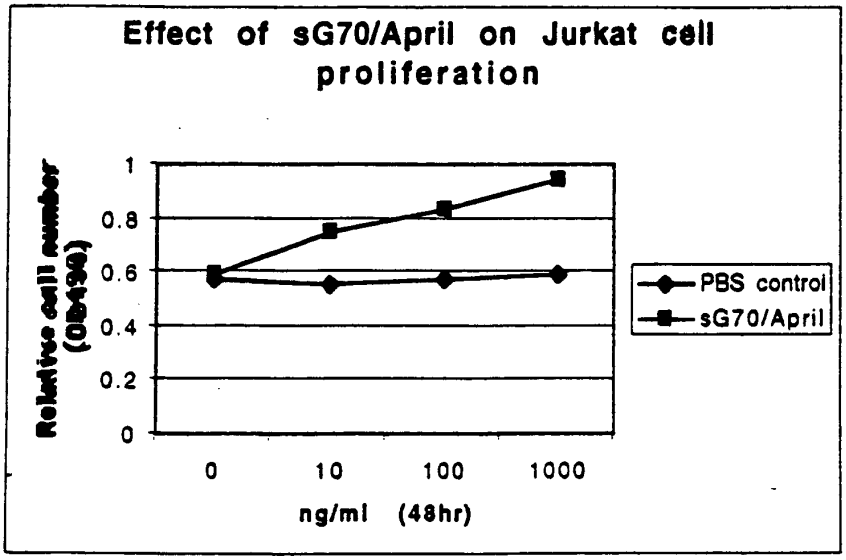
G-70 FLAG des92 (smuG70) Strain #4081 (SEQ ID NO 19):

```
MDYKDDDDKKHKKKHSVLHLVPVNITSKDSDVTEVMWQPVLRRGRGLEAQGDIVRVW
DTGIYLLYSQVLFHDVTFTMGQVVSREGQGRRETLFRCIRSMPSDPDRAYNSCYSAG
VFHLHQGDIITVKIPRANAKLSLSPHGTFLGFVKL*
```

Figure 3
Alignm. of human and mouse G70

```
mouse: 1   MPASS---------PGHMGGSVREPALSVALWLSWGAVLGAVTCAVALLIQQTELQSLRR 51
           MPASS          PG+MGG VREPALSVALWLSWGA LGAV CA+ALL QQTELQSLRR
Human: 1   MPASSPFLLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRR 60

mouse: 52  EVSRLQRSGGPSQKQGERPWQSLWEQSPDVLEAWKDGAKSRRRRAVLTQKHKKKHSVLHL 111
           EVSRLQ +GGPSQ      PWQSL EQS D LEAW+ G +SR+RRAVLTQK KK+HSVLHL
human: 61  EVSRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWESGERSRKRRAVLTQKQKKQHSVLHL 120

mouse: 112 VPVNITSKD-SDVTEVMWQPVLRRGRGLEAQGDIVRVWDTGIYLLYSQVLFHDVTFTMGQ 170
           VP+N TSKD SDVTEVMWQP LRRGRGL+AQG  VR+ D G+YLLYSQVLF DVTFTMGQ
human: 121 VPINATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

mouse: 171 VVSREGQGRRETLFRCIRSMPSDPDRAYNSCYSAGVFHLHQGDIITVKIPRANAKLSLSP 230
           VVSREGQGR+ETLFRCIRSMPS PDRAYNSCYSAGVFHLHQGDI++V IPRA AKL+LSP
human: 181 VVSREGQGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP 240

mouse: 231 HGTFLGFVKL 240
           HGTFLGFVKL
human: 241 HGTFLGFVKL 250
```


Effect of sG70/April on Raji cell proliferation
Relative cell number (OD490)
1.2
1
0.8
0.6
0.4
0.2
0
0
10
100
1000
ng/ml (48hr)
PBS control
sG70/April


Effect of sG70/April on Jurkat cell proliferation
Relative cell number (OD490)
1
0.8
0.6
0.4
0.2
0
0
10
100
1000
ng/ml (48hr)
PBS control
sG70/April

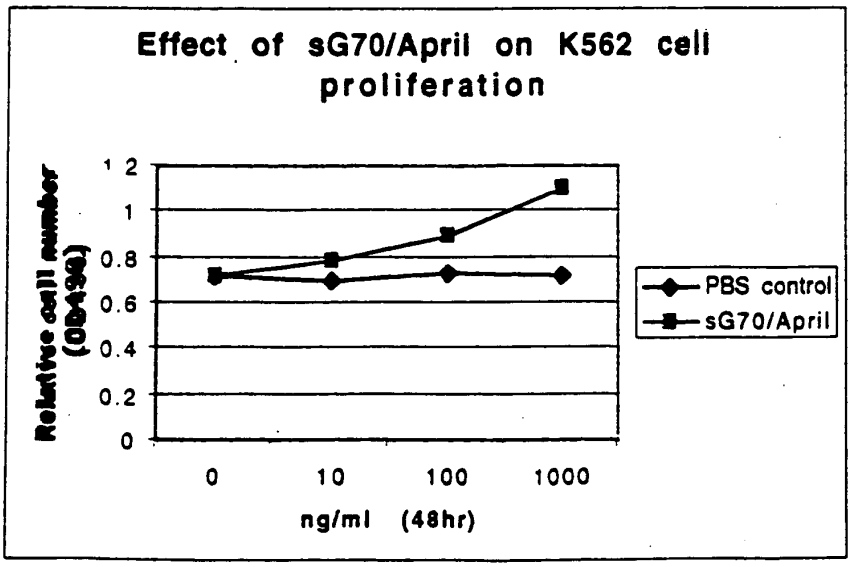
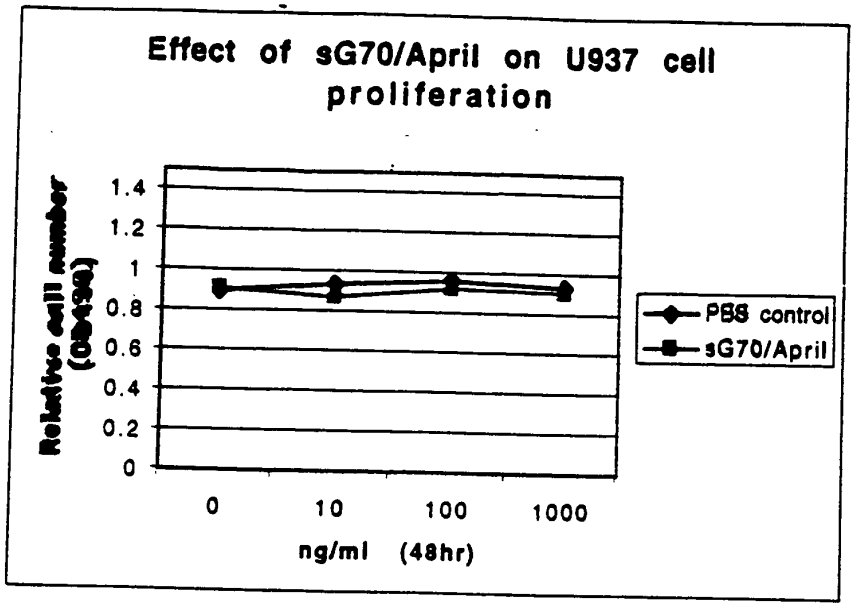
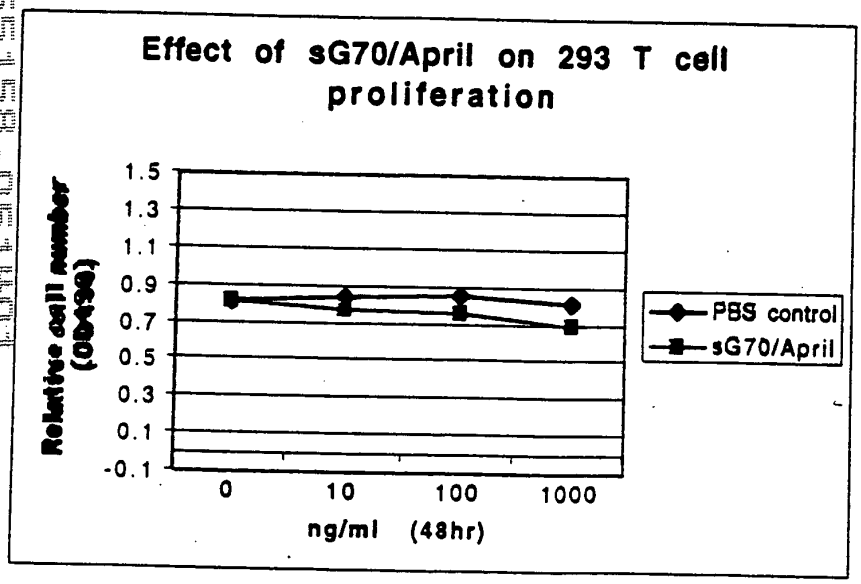

Effect of sG70/April on K562 cell proliferation
Relative cell number (OD490)
1 2
1
0.8
0.6
0.4
0.2
0
0
10
100
1000
ng/ml (48hr)
PBS control
sG70/April

Fig. 4A

Fig. 4B


Effect of sG70/April on U937 cell proliferation
Relative cell number (OD490)
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
10
100
1000
ng/ml (48hr)
PBS control
sG70/April


Effect of sG70/April on 293 T cell proliferation
Relative cell number (OD490)
1.5
1.3
1.1
0.9
0.7
0.5
0.3
0.1
-0.1
0
10
100
1000
ng/ml (48hr)
PBS control
sG70/April

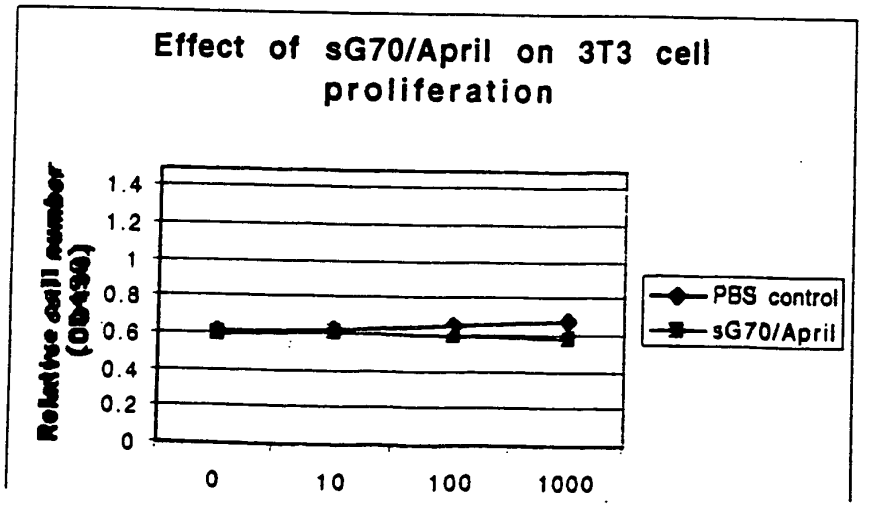
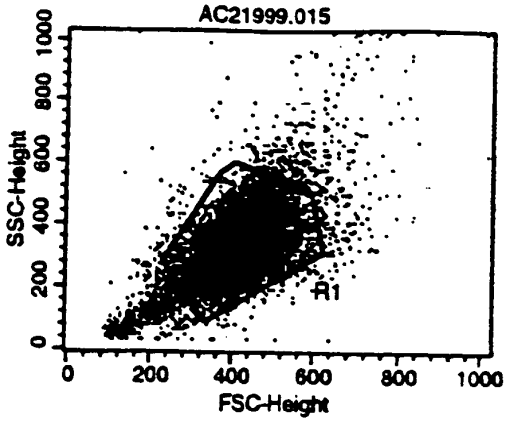
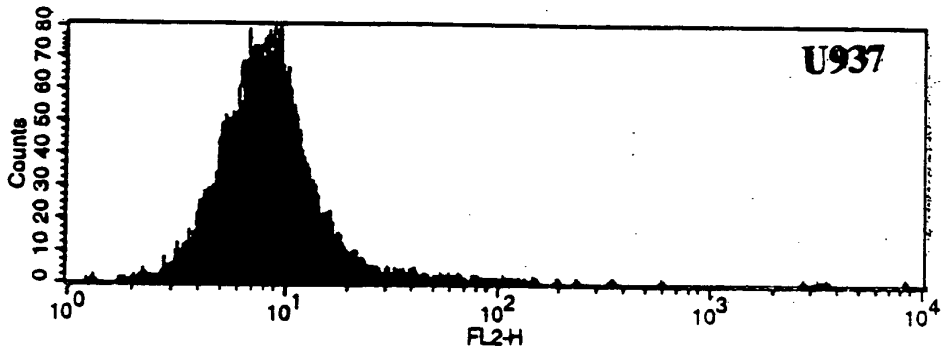
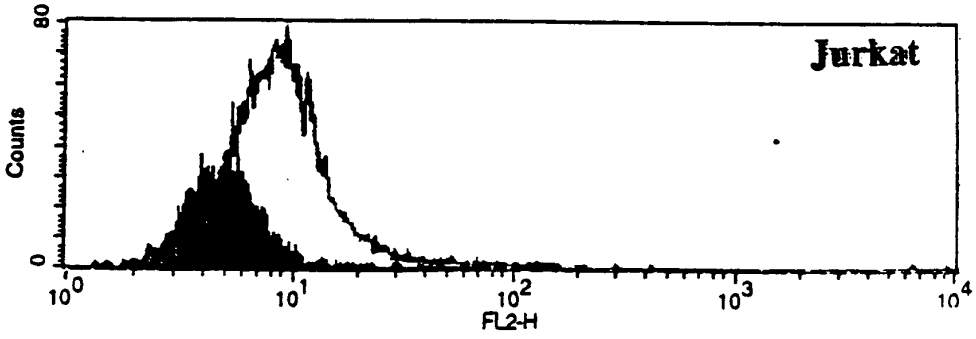

Effect of sG70/April on 3T3 cell proliferation
Relative cell number (OD490)
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
10
100
1000
PBS control
sG70/April

FIGURE 5A



FACS analysis of G70/April receptor binding





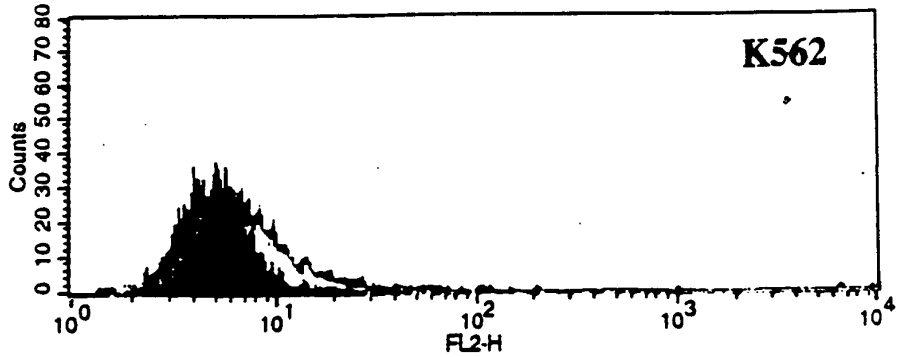
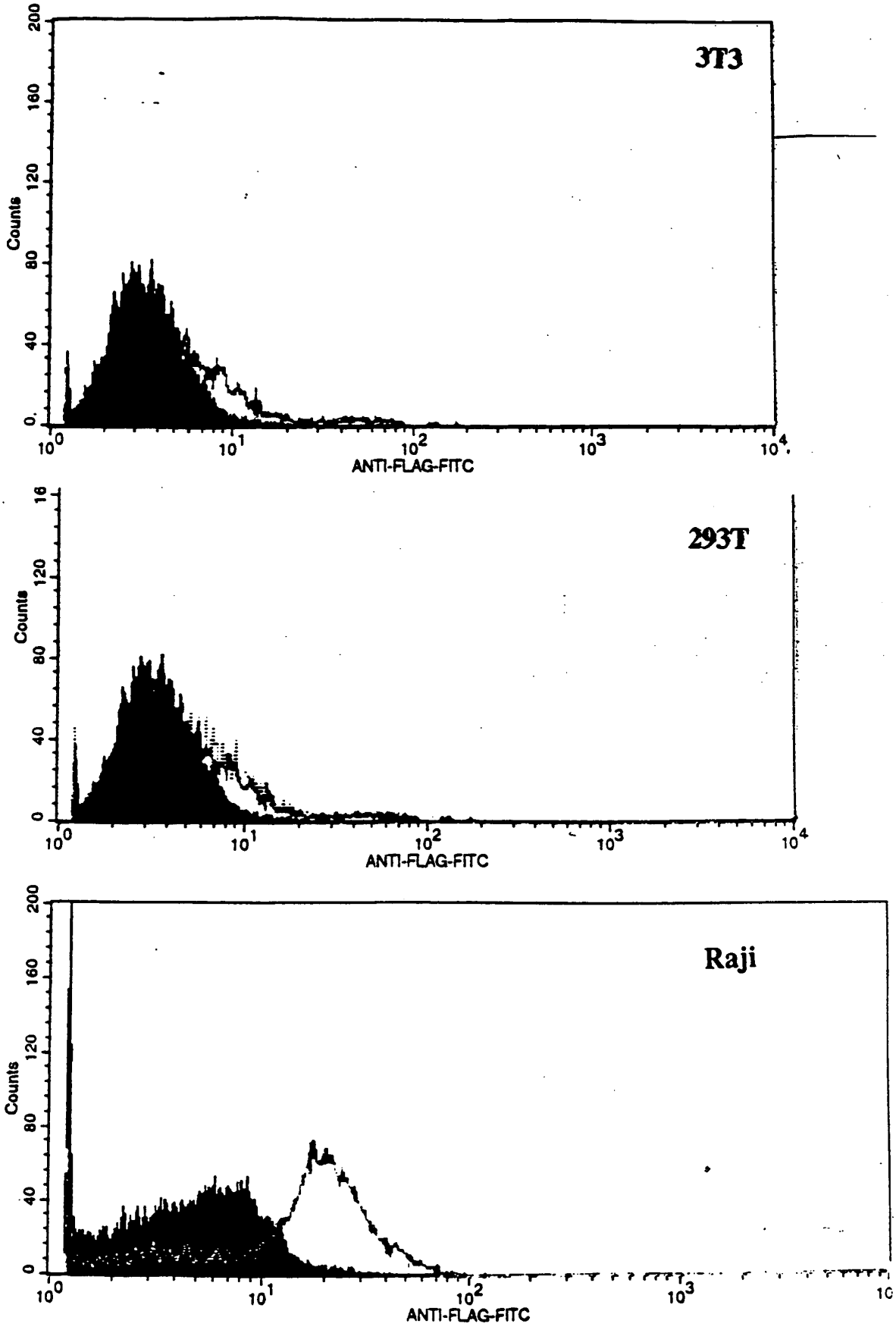


FIGURE 5B


3T3
Counts
ANTI-FLAG-FITC
293T
Counts
ANTI-FLAG-FITC
Raji
Counts
ANTI-FLAG-FITC

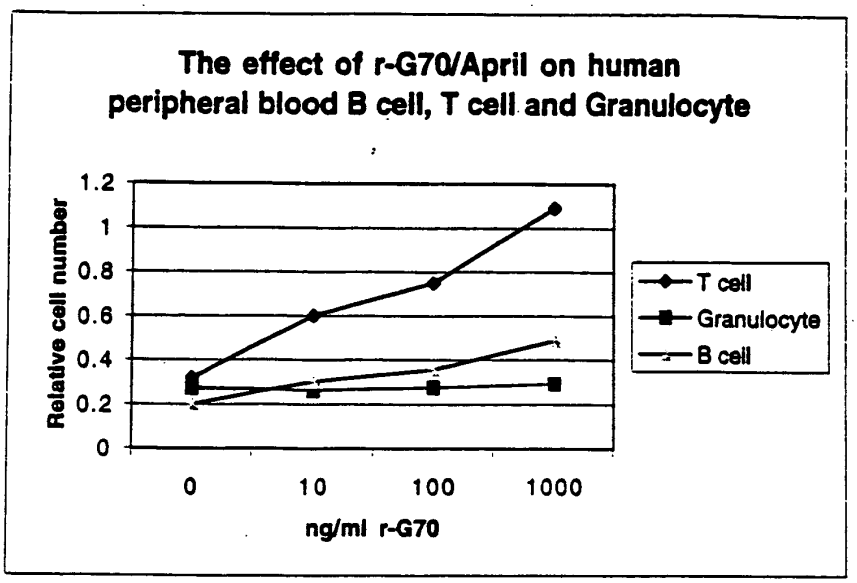
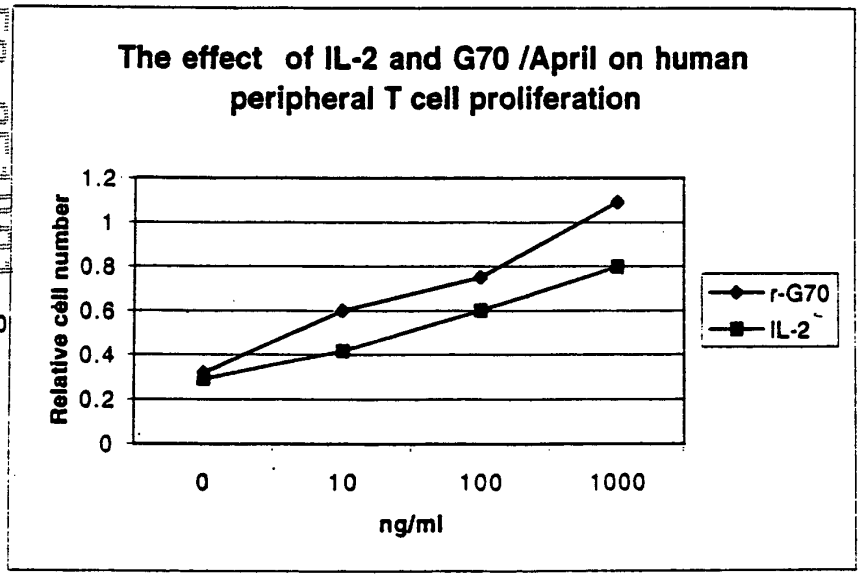
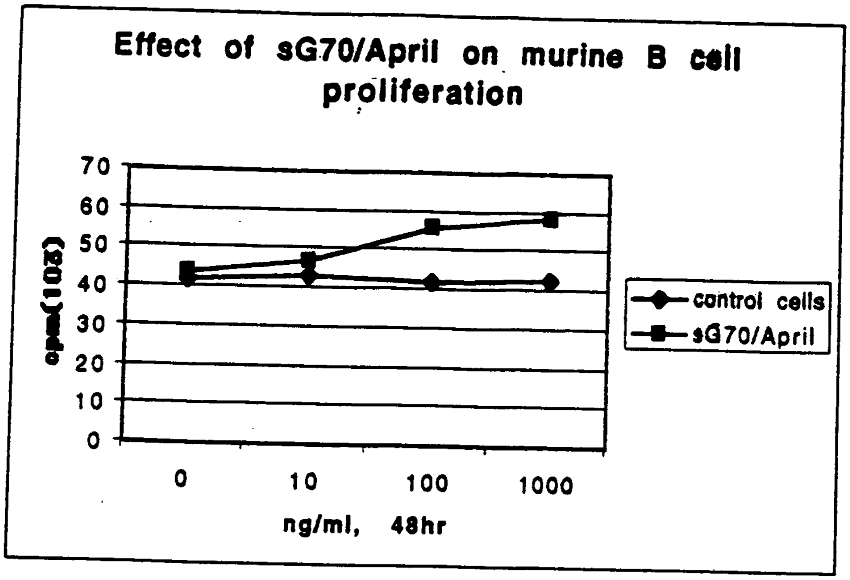

The effect of r-G70/April on human peripheral blood B cell, T cell and Granulocyte
Relative cell number
1.2
1
0.8
0.6
0.4
0.2
0
0
10
100
1000
ng/ml r-G70
T cell
Granulocyte
B cell

Fig. 6


The effect of IL-2 and G70 /April on human peripheral T cell proliferation
Relative cell number
1.2
1
0.8
0.6
0.4
0.2
0
0
10
100
1000
ng/ml
r-G70
IL-2

r-G70

Fig. 7



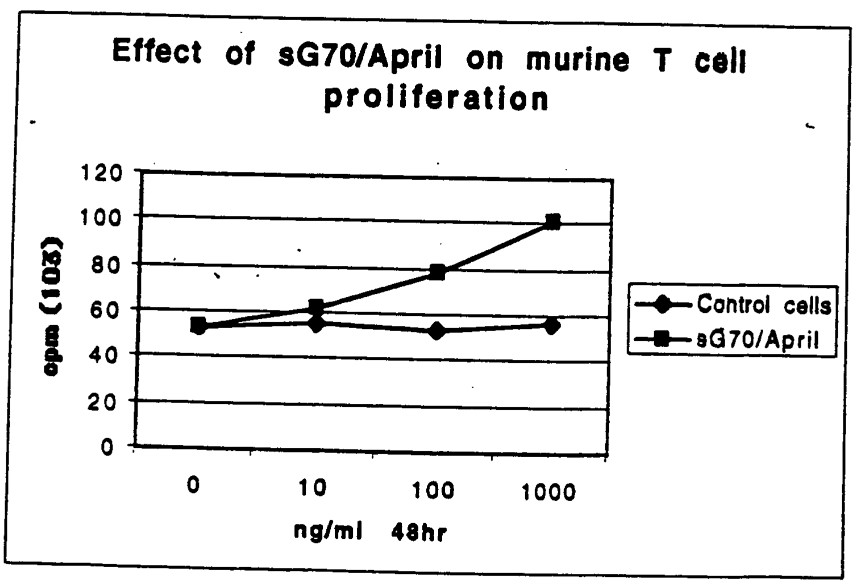


Fig. 8

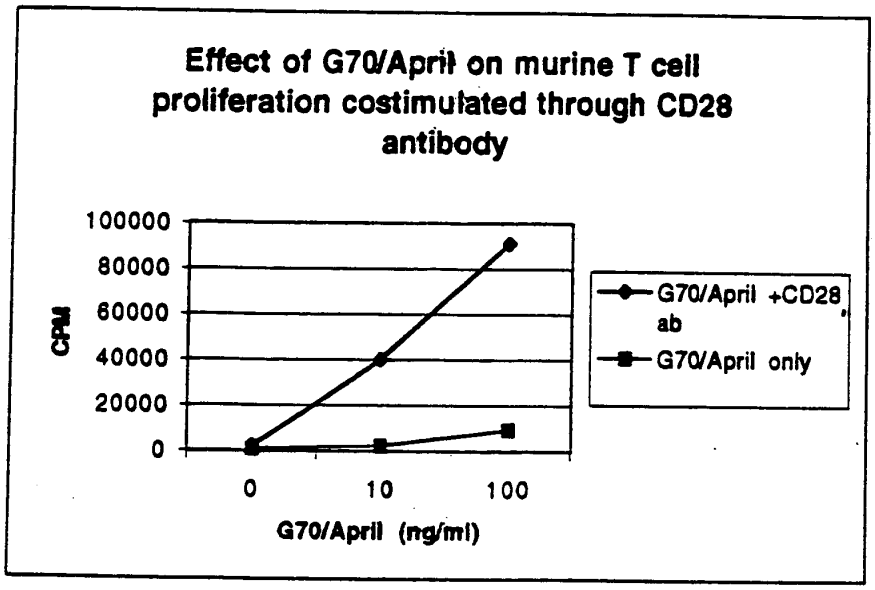

Effect of G70/April on murine T cell proliferation costimulated through CD28 antibody
CPM
100000
80000
60000
40000
20000
0
0
10
100
G70/April (ng/ml)
G70/April +CD28 ab
G70/April only

Fig. 9

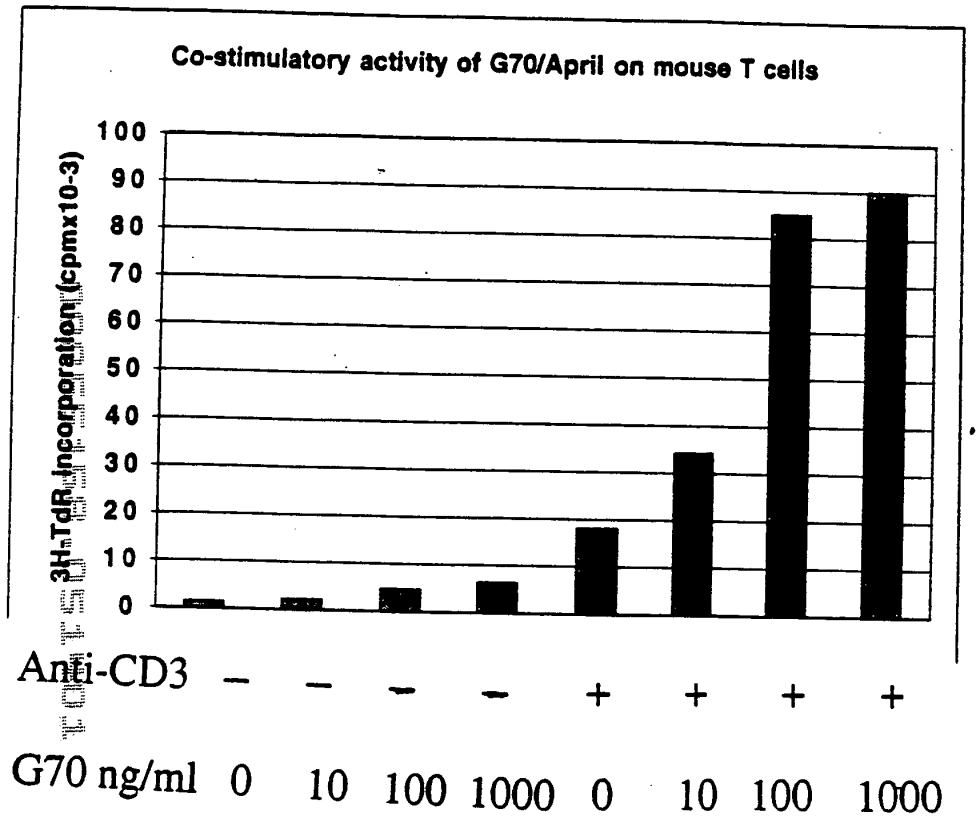

Co-stimulatory activity of G70/April on mouse T cells
3H-TdR Incorporation (cpmx10-3)
100
90
80
70
60
50
40
30
20
10
0
Anti-CD3 – – – – + + + +
G70 ng/ml 0 10 100 1000 0 10 100 1000

Figure 10A

Human BCMA

Human (SEQ ID NO: 5):

1 MAGQCSQNEY FDSLLHACIP CQLRCSSNTP PLTCQRYCNA SVTNSVKGTN

51 AILWTCLGLS LIISLAVFVL MFLLRKISSE PLKDEFKNTG SGLLGMANID

101 LEKSRTGDEI ILPRGLEYTV EECTCEDCIK SKPKVDSDHC FPLPAMEEGA

151 TILVTTKTND YCKSLPAALS ATEIEKSISA R

Human (SEQ ID NO: 5):

MAGQ**CSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY C**NASVTNSVK GTNA ILWTCL GLSLIISLAV FVLMFLLRKI SSEPLKDEFK NTGSGLLGMA NIDLEKSRTG DEIILPRGLE YTVEECTCED CIKSKPKVDS DHCFPLPAME EGATILVTTK TNDYCKSLPA ALSATEIEKS ISAR

hBCMA's extracellular domain (SEQ ID NO: 6):

MAGQCSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY CNASVTNSVK GTNA

hBCMA's cysteine-rich consensus region (SEQ ID NO: 7):

CSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY C

hBCMA's transmembrane region (SEQ ID NO: 8):

ILWTCL GLSLIISLAV FVLMF

Figure 10B

huBCMA-Fc (SEQ ID NO: 9):

MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA
GGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK*

muBCMA-Fc (SEQ ID NO: 10):

MAQQCFHSEYFDSLLHACKPCHLRCSNPPATCQPYCDPSVTSSVKGSYTG
GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK*

Figure 11
Alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence

murine BCMA amino acid sequence Length: 185 (SEQ ID NO: 11):

```
  1  MAQQCFHSEY FDSLLHACKP CHLRCSNPPA TCQPYCDPSV TSSVKGTYTV

 51  LWIFLGLTLV LSLALFTISF LLRKMNPEAL KDEPQSPGQL DGSAQLDKAD

101  TELTRIRAGD DRIFPRSLEY TVEECTCEDC VKSKPKGDSD HFFPLPAMEE

151  GATILVTTKT GDYGKSSVPT ALQSVMGMEK PTHTR
```

alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence.

```
Query:     4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
             MA QC  +EYFDSLLHAC PC LRCS+  PP TCQ YC+ SVT+SVKGT  +LW  LGL+
Sbjct:     1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58

Query:    64 LIISLAVFVLMFLLRKISSEPLKDEFKNTG----SGLLGMANIDLEKSRTGDEIILPRGL 119
             L++SLA+F + FLLRK++ E LKDE ++ G    S  L  A+ +L + R GD+ I PR L
Sbjct:    59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL 118

Query:   120 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKS-LPAAL-SATEI 177
             EYTVEECTCEDC+KSKPK DSDH FPLPAMEEGATILVTTKT DY KS +P AL S   +
Sbjct:   119 EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM 178

Query:   178 EKSISAR 184
             EK    R
Sbjct:   179 EKPTHTR 185
```

Figure 12A

Human TACI

huTACI (SEQ ID NO: 14).

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC

51 KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC

101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL

151 PGLKLSADQV ALVYSTLGLC LCAVLCCFLV AVACFLKKRG DPCSCQPRSR

201 PRQSPAKSSQ DHAMEAGSPV STSPEPVETC SFCFPECRAP TQESAVTPGT

251 PDPTCAGRWG CHTRTTVLQP CPHIPDSGLG IVCVPAQEGG PGA

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSC
KTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQC
AYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPAL
PGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSR
PRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAPTQESAVTPGT
PDPTCAGRWGCHTRTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

huTACI's extracellular domain (SEQ ID NO: 15):

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC

51 KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC

101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL

151 PGLKLSADQV ALVYST

Figure 12B

huTACI's cysteine-rich consensus region (SEQ ID NO: 16):
CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC and
CRKEQGKFYDHLLRDCISCASICGQHPKQCAYFC

transmembrane region (SEQ ID NO: 17):
LGLCLCAVLCCFLVAVACFL

hTACI-Fc (SEQ ID NO: 18):

```
1   MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC

      51  KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC

     101  AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL

     151  PGLKLSADQV ALVYSGGGGG DKTHTCPPCP APELLGGPSV FLFPPKPKDT

     201  LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY

     251  RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT

     301  LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS

     351  DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK*
```

Figure 13

Alignment of cysteine rich extracellular regions of human TACI and human BCMA.

```
34 CPEEQYWDPLLGTCMSCKTICNHQS.QRTCAAFCRSLSCRKEQGKFYDHL 82
   | : :|.| ||  |. |.  |.  .   ||  :| .      .|   . :
 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT..NAI 55

83 LRDCISCASI 92
   |  |:  . |
56 LWTCLGLSLI 65
```

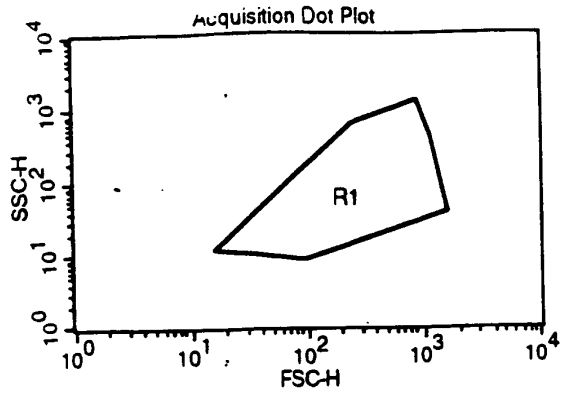
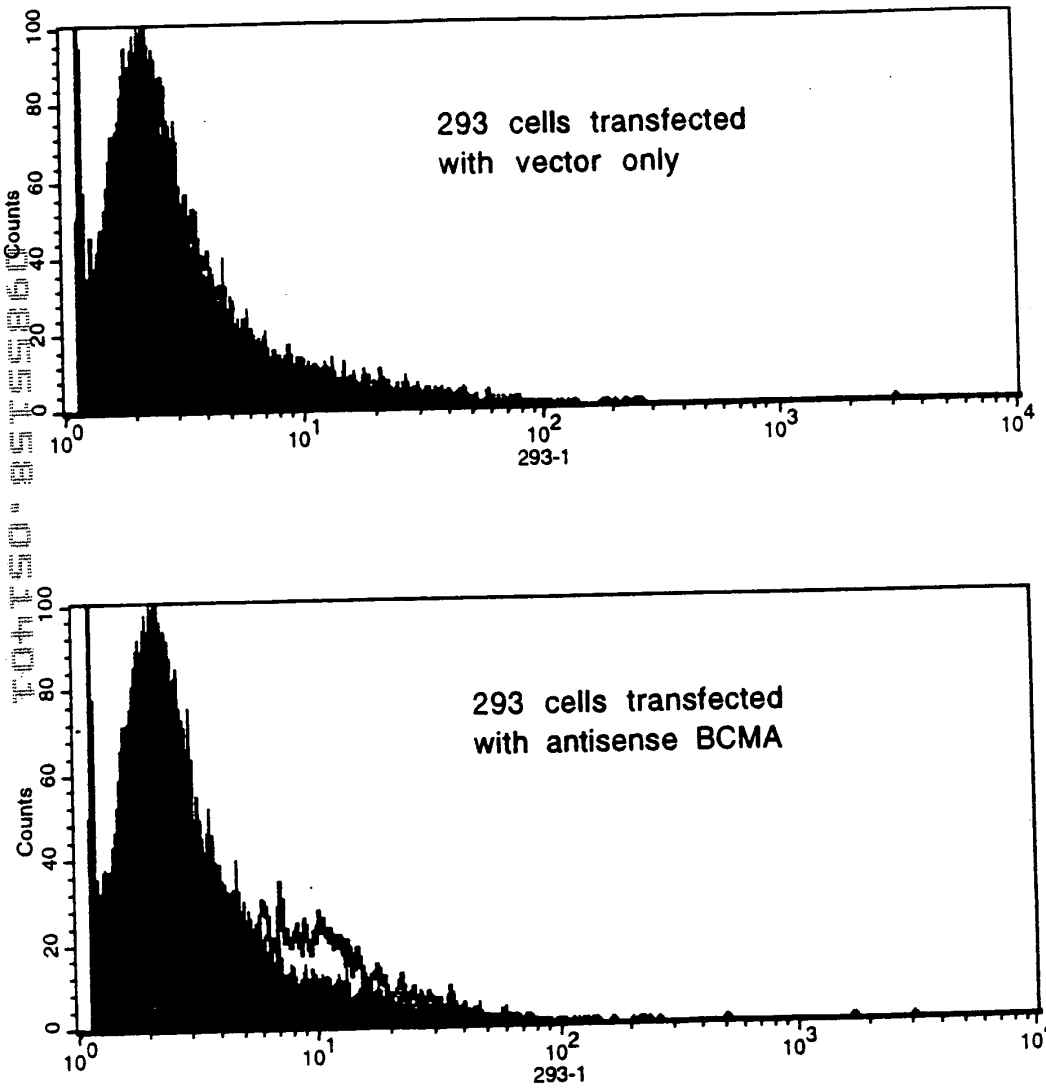

Acquisition Dot Plot
SSC-H
FSC-H
R1

Fig.14


A.
293 cells transfected
with vector only
Counts
293-1
B.
293 cells transfected
with antisense BCMA
Counts
293-1

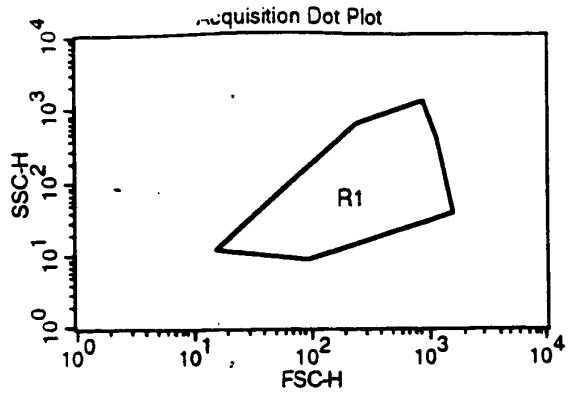
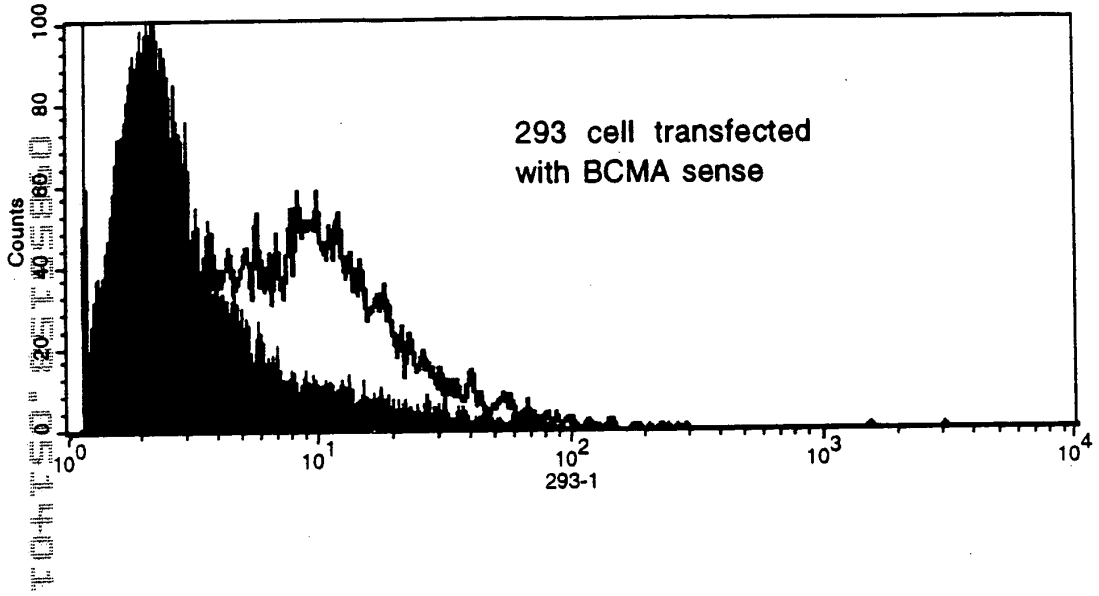

Acquisition Dot Plot
SSC-H
FSC-H
R1

Fig.14

C.


293 cell transfected
with BCMA sense
Counts
293-1

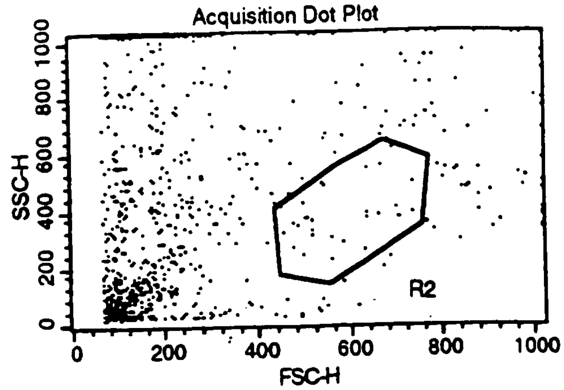
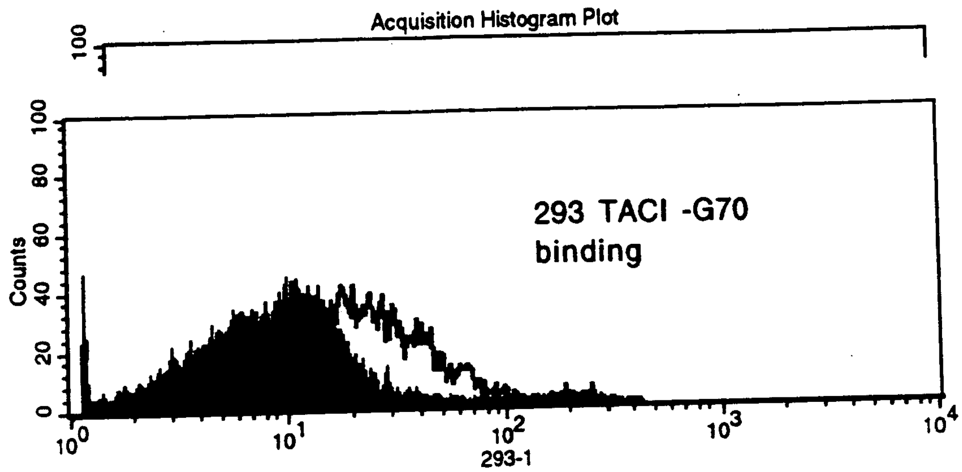
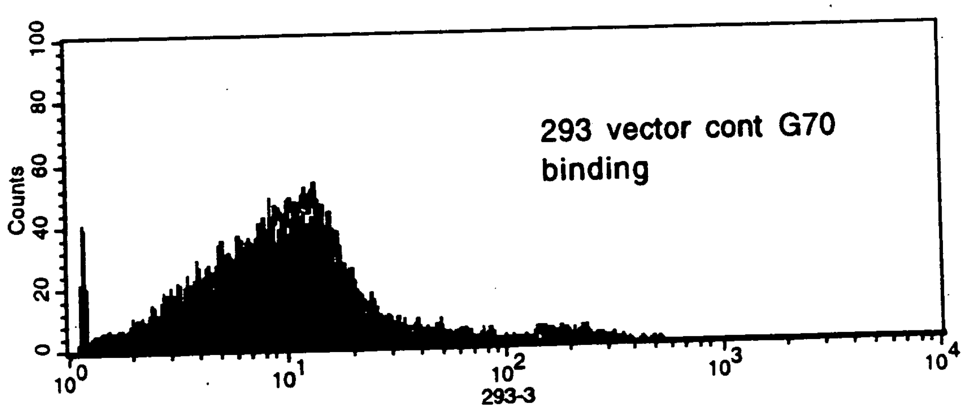


Fig. 15



A.



B.

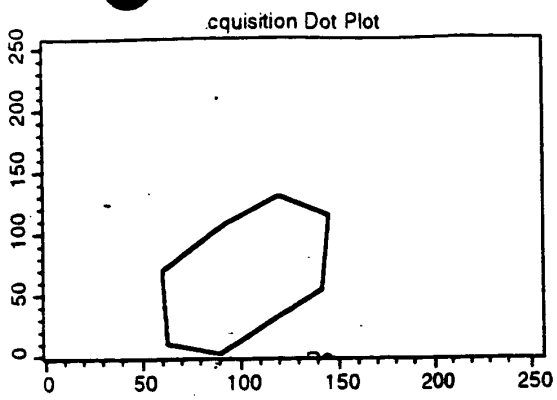
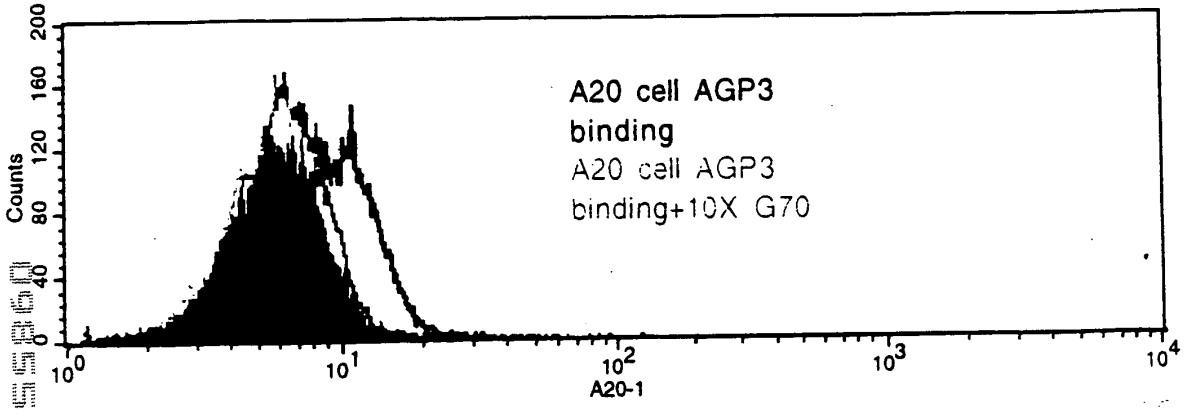
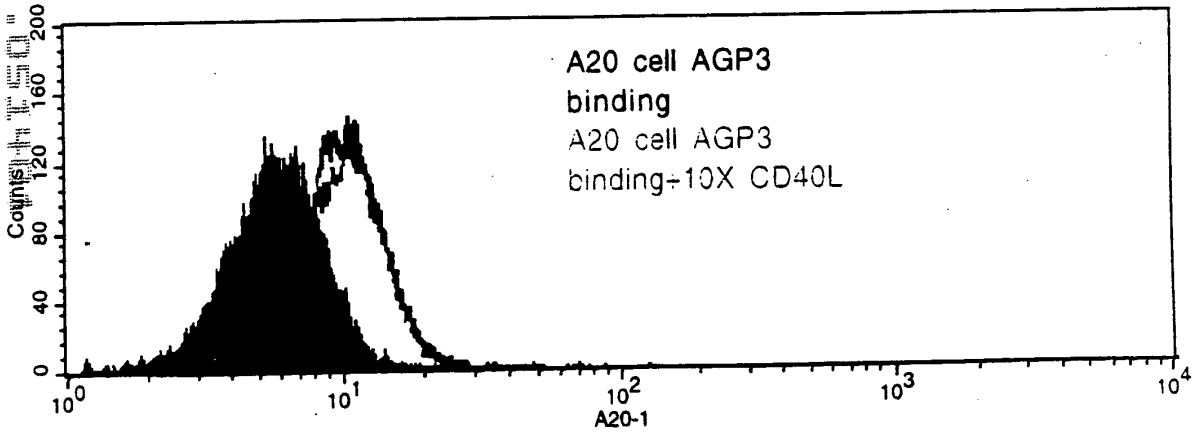


Fig. 16

A.



B.



Experiment 4-3-2000

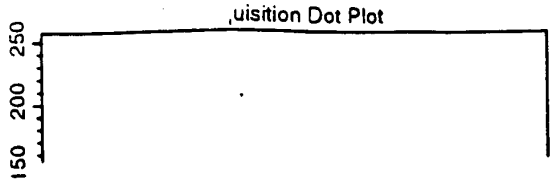
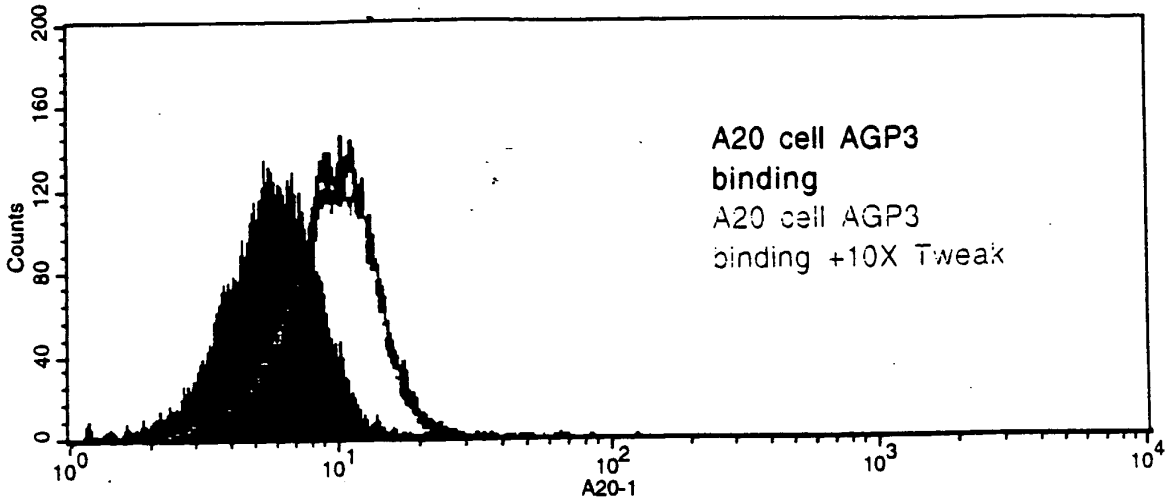
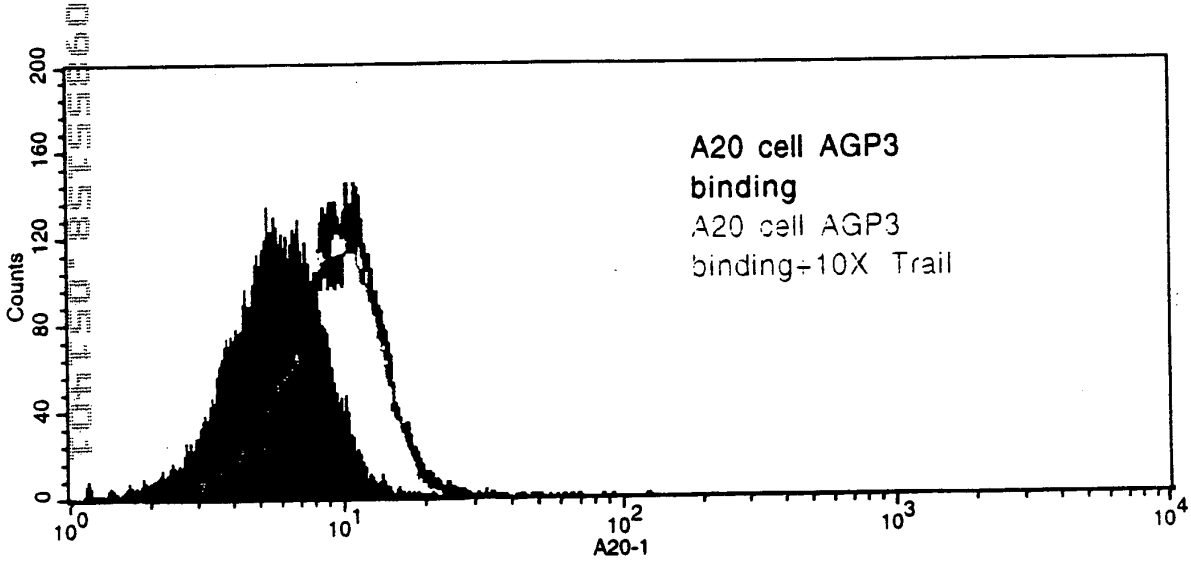


Fig. 16

C.

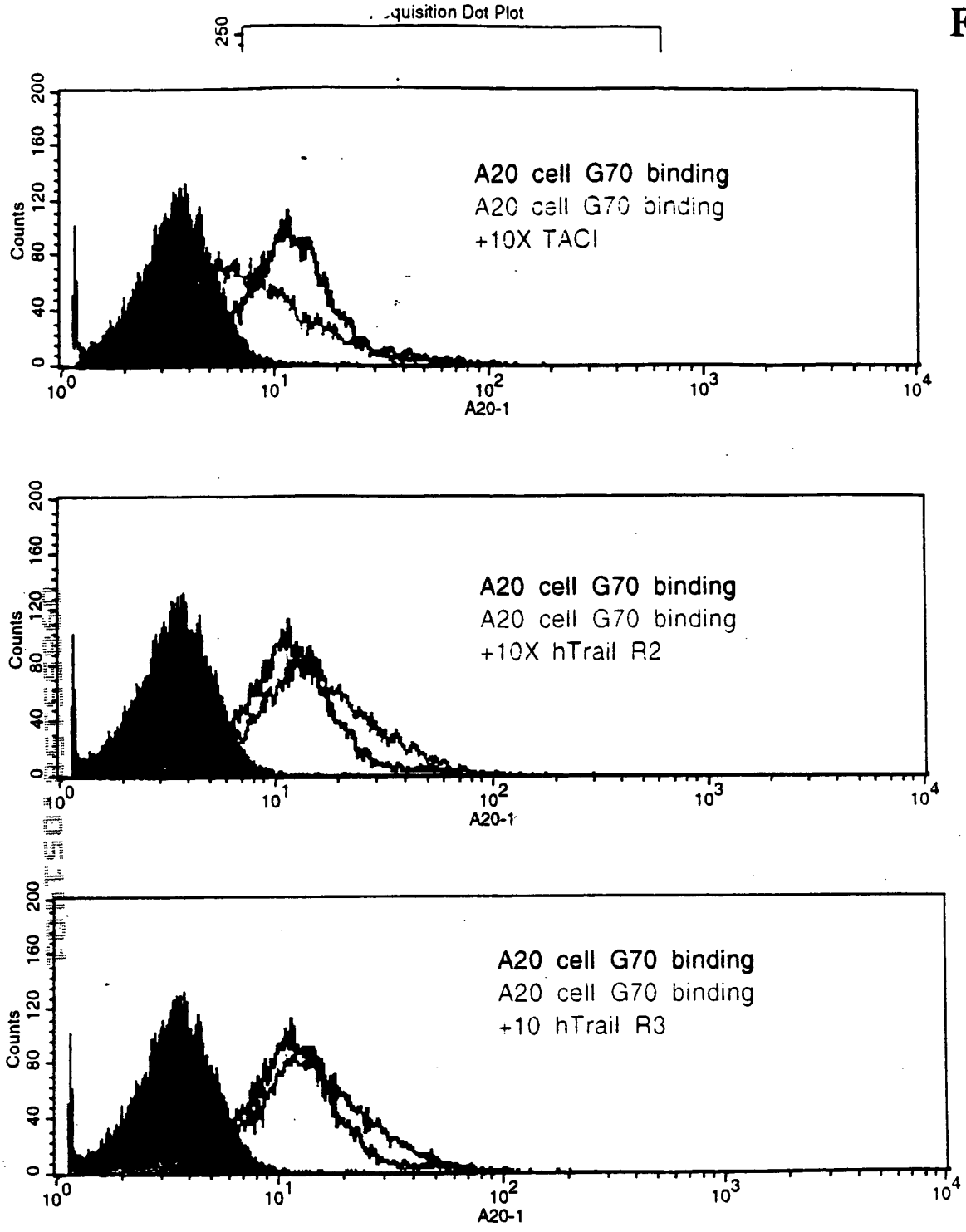


D.



Experiment 4-3-2000

Fig.17



Experiment
4-11-2000

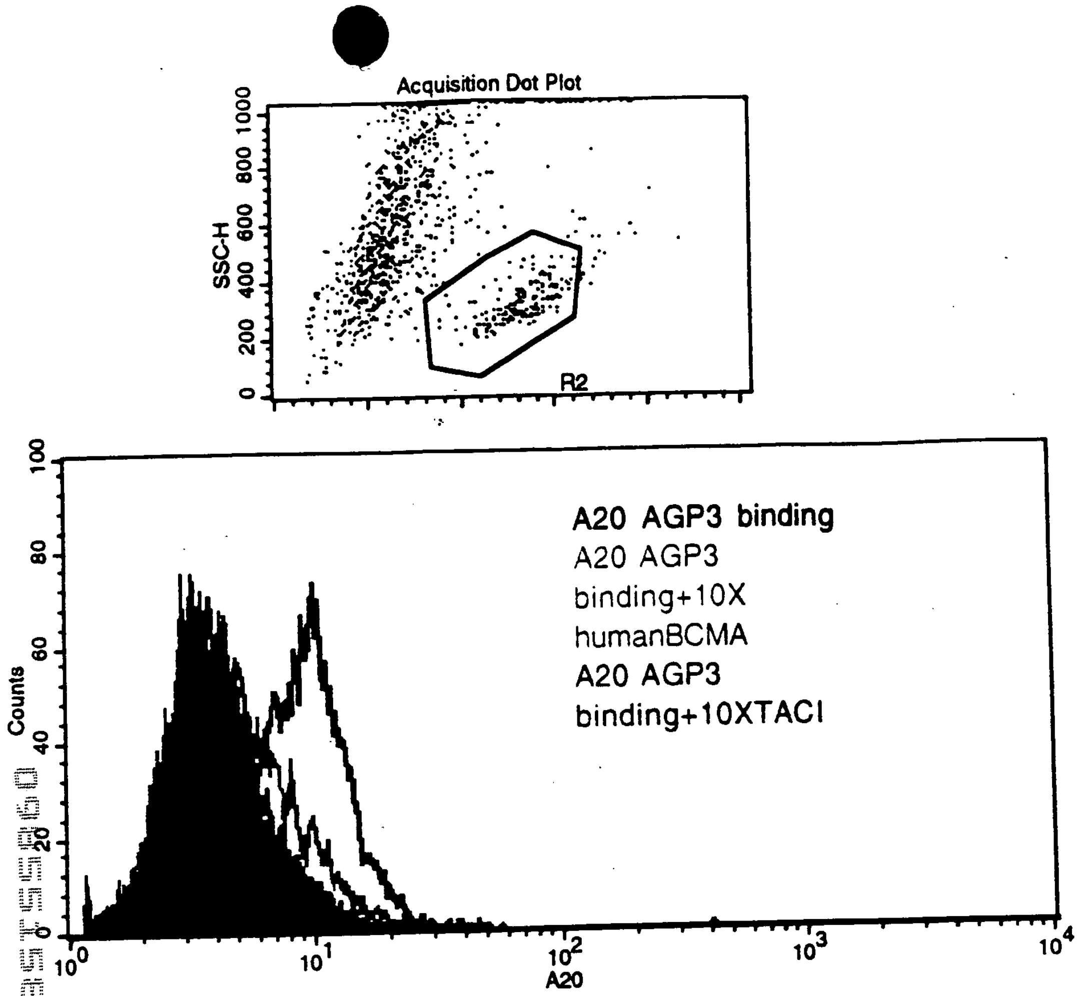
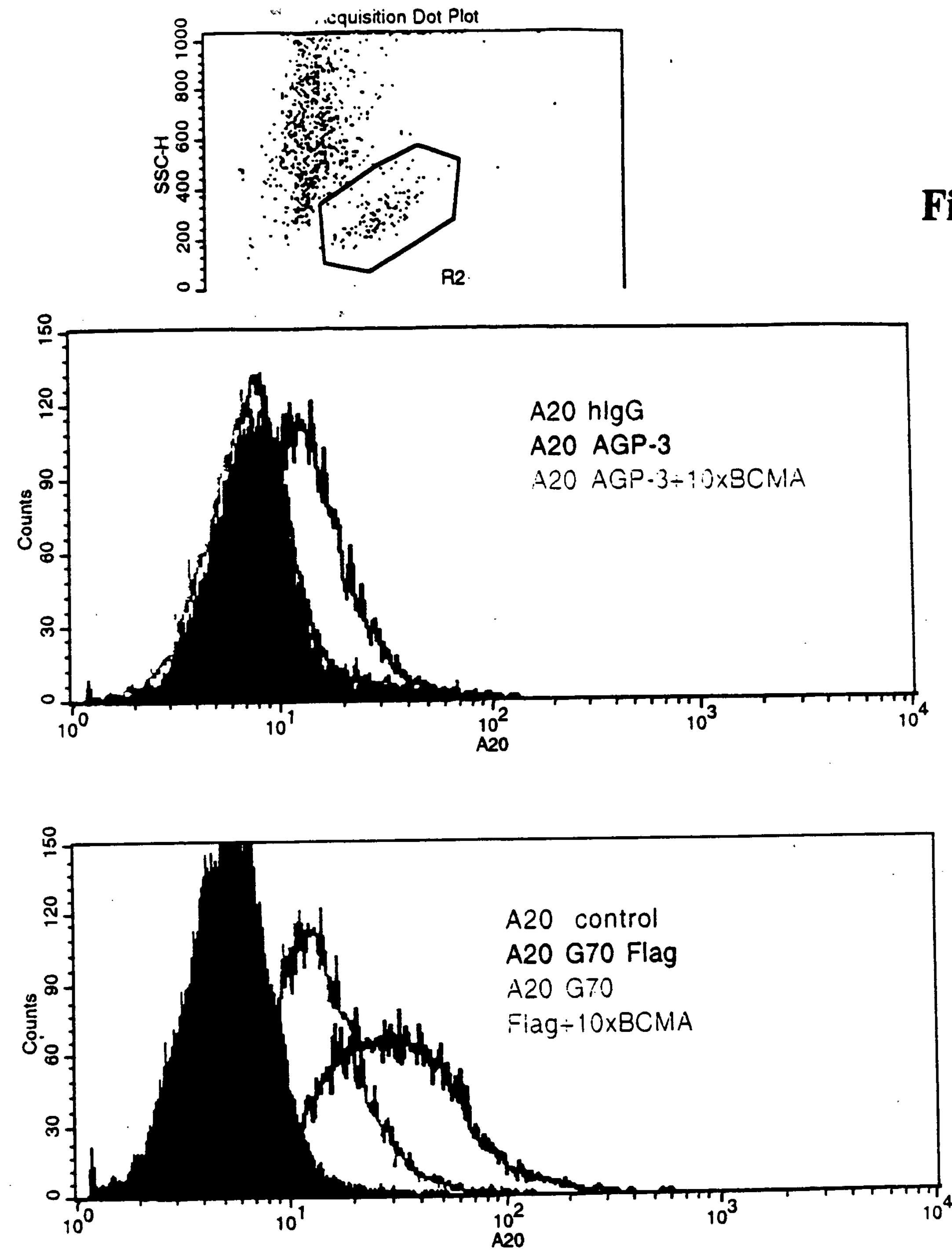

Acquisition Dot Plot
SSC-H
0
200
400
600
800
1000
R2
Counts
0
20
40
60
80
100
A20 AGP3 binding
A20 AGP3
binding+10X
humanBCMA
A20 AGP3
binding+10XTACI
10^0
10^1
10^2
10^3
10^4
A20

Fig.18

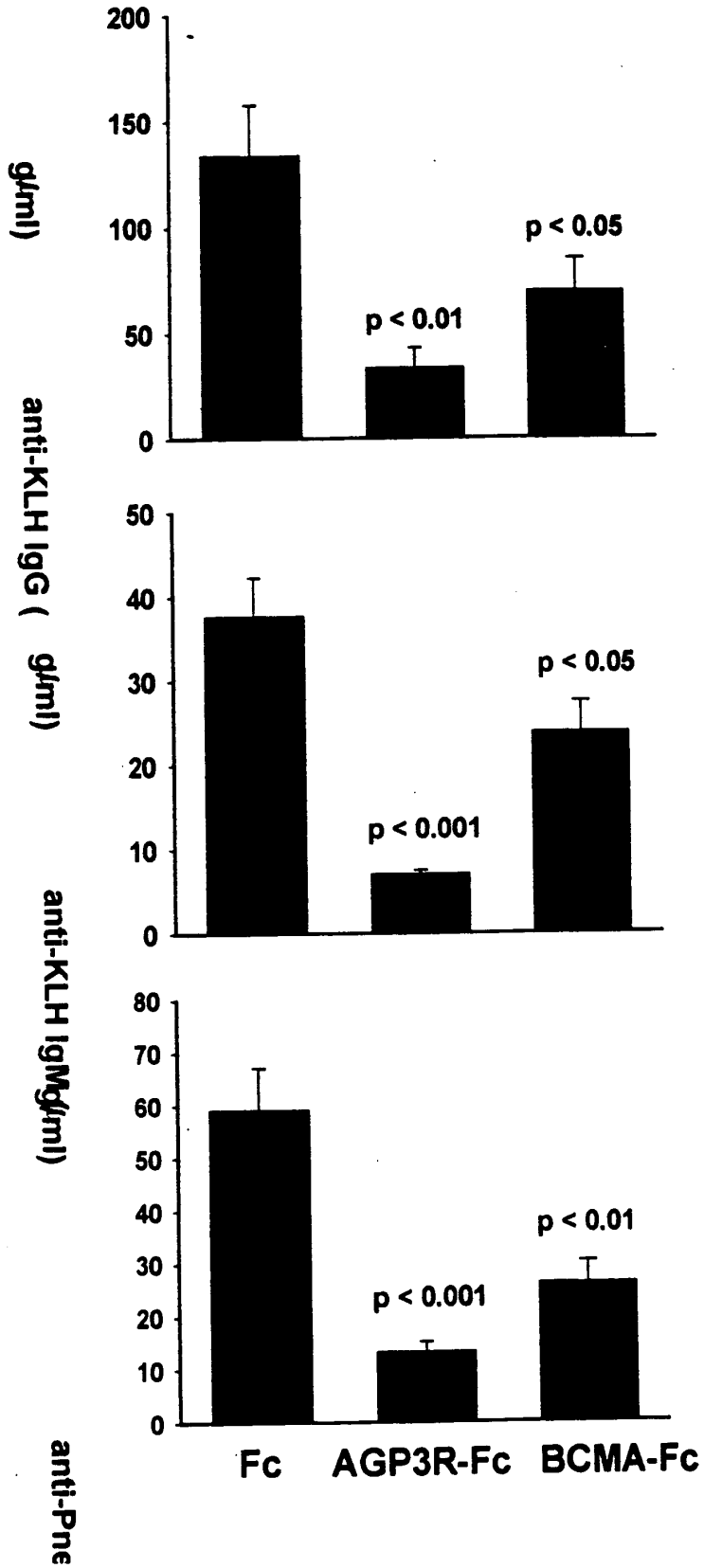
Fig.19


Acquisition Dot Plot
SSC-H
R2
A20 hIgG
A20 AGP-3
A20 AGP-3+10xBCMA
Counts
A20
A20 control
A20 G70 Flag
A20 G70
Flag+10xBCMA
Counts
A20

A.

B.

Fig.20


A
B
C
anti-KLH IgG (g/ml)
anti-KLH IgM g/ml)
anti-Pne
200
150
100
50
0
p < 0.01
p < 0.05
50
40
30
20
10
0
p < 0.001
p < 0.05
80
70
60
50
40
30
20
10
0
p < 0.001
p < 0.01
Fc
AGP3R-Fc
BCMA-Fc